



Figure S1. Performance comparison for generation of the mutation spectra matrix from a MAF input file. For Helmsman and two other MAF-specific mutation signature analysis tools (maftools and Mutation-Signatures), we measured the maximum memory usage in megabytes (a) and processing time in seconds (b) required to generate the 377 x 96 mutation spectra matrix from a MAF file containing 60,691 SNVs (in addition to 1,415,224 non-SNV variants that were present in the file but not analyzed) in 377 samples from The Cancer Genome Atlas.